

## (ix) TELECOMMUNICATION INFORMATION:

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(B) TELEFAX: 206-442-6678

(C) TELEX:

## (2) INFORMATION FOR SEQ ID NO:1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1733 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

## (ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 34...1344

(D) OTHER INFORMATION:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCGACCCAC GCGTCCGCAG CCACAGACGG GTC ATG AGC GCG GTA TTA CTG CTG	54
Met Ser Ala Val Leu Leu Leu	
1 5	
GCC CTC CTG GGG TTC ATC CTC CCA CTG CCA GGA GTG CAG GCG CTG CTC	102
Ala Leu Leu Gly Phe Ile Leu Pro Leu Pro Gly Val Gln Ala Leu Leu	
10 15 20	
TGC CAG TTT GGG ACA GTT CAG CTT GTG TGG AAG GTG TCC GAC CTA CCC	150
Cys Gln Phe Gly Thr Val Gln Leu Val Trp Lys Val Ser Asp Leu Pro	
25 30 35	
CGG CAA TGG ACC CCT AAG AAC ACC AGC TGC GAC AGC GGC TTG GGG TGC	198
Arg Gln Trp Thr Pro Lys Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys	
40 45 50 55	
CAG GAC ACG TTG ATG CTC ATT GAG AGC GGA CCC CAA GTG AGC CTG GTG	246
Gln Asp Thr Leu Met Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val	
60 65 70	

CTC	TCC	AAG	GGC	TGC	ACG	GAG	GCC	AAG	GAC	CAG	GAG	CCC	CGC	GTC	ACT	294
Leu	Ser	Lys	Gly	Cys	Thr	Glu	Ala	Lys	Asp	Gln	Glu	Pro	Arg	Val	Thr	
			75					80					85			
GAG	CAC	CGG	ATG	GGC	CCC	GGC	CTC	TCC	CTG	ATC	TCC	TAC	ACC	TTC	GTG	342
Glu	His	Arg	Met	Gly	Pro	Gly	Leu	Ser	Leu	Ile	Ser	Tyr	Thr	Phe	Val	
		90					95					100				
TGC	CGC	CAG	GAG	GAC	TTC	TGC	AAC	AAC	CTC	GTT	AAC	TCC	CTC	CCG	CTT	390
Cys	Arg	Gln	Glu	Asp	Phe	Cys	Asn	Asn	Leu	Val	Asn	Ser	Leu	Pro	Leu	
	105					110					115					
TGG	GCC	CCA	CAG	CCC	CCA	GCA	GAC	CCA	GGA	TCC	TTG	AGG	TGC	CCA	GTC	438
Trp	Ala	Pro	Gln	Pro	Pro	Ala	Asp	Pro	Gly	Ser	Leu	Arg	Cys	Pro	Val	
120					125				130						135	
TGC	TTG	TCT	ATG	GAA	GGC	TGT	CTG	GAG	GGG	ACA	ACA	GAA	GAG	ATC	TGC	486
Cys	Leu	Ser	Met	Glu	Gly	Cys	Leu	Glu	Gly	Thr	Thr	Glu	Glu	Ile	Cys	
			140					145						150		
CCC	AAG	GGG	ACC	ACA	CAC	TGT	TAT	GAT	GGC	CTC	CTC	AGG	CTC	AGG	GGA	534
Pro	Lys	Gly	Thr	Thr	His	Cys	Tyr	Asp	Gly	Leu	Leu	Arg	Leu	Arg	Gly	
			155					160					165			
GGA	GGC	ATC	TTC	TCC	AAT	CTG	AGA	GTC	CAG	GGA	TGC	ATG	CCC	CAG	CCA	582
Gly	Gly	Ile	Phe	Ser	Asn	Leu	Arg	Val	Gln	Gly	Cys	Met	Pro	Gln	Pro	
		170					175					180				
GGT	TGC	AAC	CTG	CTC	AAT	GGG	ACA	CAG	GAA	ATT	GGG	CCC	GTG	GGT	ATG	630
Gly	Cys	Asn	Leu	Leu	Asn	Gly	Thr	Gln	Glu	Ile	Gly	Pro	Val	Gly	Met	
	185					190					195					
ACT	GAG	AAC	TGC	AAT	AGG	AAA	GAT	TTT	CTG	ACC	TGT	CAT	CGG	GGG	ACC	678
Thr	Glu	Asn	Cys	Asn	Arg	Lys	Asp	Phe	Leu	Thr	Cys	His	Arg	Gly	Thr	
200					205					210					215	
ACC	ATT	ATG	ACA	CAC	GGA	AAC	TTG	GCT	CAA	GAA	CCC	ACT	GAT	TGG	ACC	726
Thr	Ile	Met	Thr	His	Gly	Asn	Leu	Ala	Gln	Glu	Pro	Thr	Asp	Trp	Thr	
				220				225						230		
ACA	TCG	AAT	ACC	GAG	ATG	TGC	GAG	GTG	GGG	CAG	GTG	TGT	CAG	GAG	ACG	774
Thr	Ser	Asn	Thr	Glu	Met	Cys	Glu	Val	Gly	Gln	Val	Cys	Gln	Glu	Thr	
			235					240						245		

CTG CTG CTC ATA GAT GTA GGA CTC ACA TCA ACC CTG GTG GGG ACA AAA	822
Leu Leu Leu Ile Asp Val Gly Leu Thr Ser Thr Leu Val Gly Thr Lys	
250 255 260	
GGC TGC AGC ACT GTT GGG GCT CAA AAT TCC CAG AAG ACC ACC ATC CAC	870
Gly Cys Ser Thr Val Gly Ala Gln Asn Ser Gln Lys Thr Thr Ile His	
265 270 275	
TCA GCC CCT CCT GGG GTG CTT GTG GCC TCC TAT ACC CAC TTC TGC TCC	918
Ser Ala Pro Pro Gly Val Leu Val Ala Ser Tyr Thr His Phe Cys Ser	
280 285 290 295	
TCG GAC CTG TGC AAT AGT GCC AGC AGC AGC AGC GTT CTG CTG AAC TCC	966
Ser Asp Leu Cys Asn Ser Ala Ser Ser Ser Ser Val Leu Leu Asn Ser	
300 305 310	
CTC CCT CCT CAA GCT GCC CCT GTC CCA GGA GAC CGG CAG TGT CCT ACC	1014
Leu Pro Pro Gln Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr	
315 320 325	
TGT GTG CAG CCC CTT GGA ACC TGT TCA AGT GGC TCC CCC CGA ATG ACC	1062
Cys Val Gln Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr	
330 335 340	
TGC CCC AGG GGC GCC ACT CAT TGT TAT GAT GGG TAC ATT CAT CTC TCA	1110
Cys Pro Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser	
345 350 355	
GGA GGT GGG CTG TCC ACC AAA ATG AGC ATT CAG GGC TGC GTG GCC CAA	1158
Gly Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln	
360 365 370 375	
CCT TCC AGC TTC TTG TTG AAC CAC ACC AGA CAA ATC GGG ATC TTC TCT	1206
Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe Ser	
380 385 390	
GCG CGT GAG AAG CGT GAT GTG CAG CCT CCT GCC TCT CAG CAT GAG GGA	1254
Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His Glu Gly	
395 400 405	
GGT GGG GCT GAG GGC CTG GAG TCT CTC ACT TGG GGG GTG GGG CTG GCA	1302
Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val Gly Leu Ala	
410 415 420	

CTG GCC CCA GCG CTG TGG TGG AGA GTG GTT TGC CCT TCC TGC TAACTCTAT 1353  
 Leu Ala Pro Ala Leu Trp Trp Arg Val Val Cys Pro Ser Cys  
           425                                  430                                  435

TACCCCCACG ATTCTTCACC GCTGCTGACC ACCCACACTC AACCTCCCTC TGACCTCATA 1413  
 ACCTAATGGC CTTGGACACC AGATTCTTTC CCATTCTGTC CATGAATCAT CTTCCCCACA 1473  
 CACAATCATT CATATCTATT CACCTAACAG CAACACTGGG GAGAGCCTGG AGCATCCGGA 1533  
 CTTGCCCTAT GGGAGAGGGG ACGCTGGAGG AGTGGCTGCA TGTATCTGAT AATACAGACC 1593  
 CTGTCCTTTC TCCCAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1653  
 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1713  
 AAAAAAAAAA GGGCGGCCGC 1733

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Ala Val Leu Leu Leu Ala Leu Leu Gly Phe Ile Leu Pro Leu  
 1                                  5                                  10                                  15  
 Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln Leu Val  
                                   20                                  25                                  30  
 Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys Asn Thr Ser  
                                   35                                  40                                  45  
 Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met Leu Ile Glu Ser  
                                   50                                  55                                  60  
 Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly Cys Thr Glu Ala Lys  
 65                                  70                                  75                                  80  
 Asp Gln Glu Pro Arg Val Thr Glu His Arg Met Gly Pro Gly Leu Ser  
                                   85                                  90                                  95  
 Leu Ile Ser Tyr Thr Phe Val Cys Arg Gln Glu Asp Phe Cys Asn Asn  
                                   100                                  105                                  110  
 Leu Val Asn Ser Leu Pro Leu Trp Ala Pro Gln Pro Pro Ala Asp Pro  
                                   115                                  120                                  125  
 Gly Ser Leu Arg Cys Pro Val Cys Leu Ser Met Glu Gly Cys Leu Glu  
                                   130                                  135                                  140  
 Gly Thr Thr Glu Glu Ile Cys Pro Lys Gly Thr Thr His Cys Tyr Asp  
 145                                  150                                  155                                  160